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Db      298 CTCTTTATGCCACGTGAGGATACAGCAAGGCCCAATCTGCAAGCCAGCAAGTCTGTC 239
QY      121 CGAGAACCAGACCATGCGAGGAAGTCTGATCGTGGACATTTACCTCCAGAACTGTGATC 180
Db      238 CGAGAACCAGACCATGCGAGGAAGTCTGATCGTGGACATTTCAACCTCCAGAACTGTGATC 179
QY      181 CAAAATGCATATGTATCTTTGGAAGAACTCTGAAGTAAAGGCCGGAATATTCTTTGTTT 240
Db      178 CAAAATGCATATGTATCTTTGGAAGAACTCTGAAGTAAAGGCCGGAATATTCTTTGTTT 119
QY      241 AAAACATTAAAAACAAACAGCAGCAAGCAAGAAGTTTCTGGCAATAAACTA 300
Db      118 AAAACATTAAAAACAAACAGCAGCAAGCAAGAAGTTTCTGGCAATAAACTA 59
QY      301 AGCACAGCCTTTTAAAAAGGAACACAAATTAAGTGTCAACCTGTGGCAAAATTTGT 358
Db      58 AGCACAGCCTTTTAAAAAGGAACACAAATTAAGTGTCAACCTGTGGCAAAATTTGT 1

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RESULT 4

ABN96147/c

ID ABN96147 standard; DNA; 176 BP.

XX

AC ABN96147;

XX

DT 13-AUG-2002 (first entry)

XX

DE Gene #2645 used to diagnose liver cancer.

XX

KW Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;

KW metastatic liver tumour; cytostatic; expression profile; disease state;

KW disease progression; drug toxicity; drug efficacy; drug metabolism.

XX

OS Homo sapiens.

XX

PN WO200229103-A2.

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PD 11-APR-2002.

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PF 02-OCT-2001; 2001WO-US030589.

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PR 02-OCT-2000; 2000US-0237054P.

XX

PA (GENE-) GENE LOGIC INC.

XX

PI Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;

XX

DR WPI; 2002-426119/45.

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PT Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in a liver tissue sample.

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PS Claim 1; SEQ ID NO 2645; 298pp; English.

XX

CC The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN93503-ABN97455 in a tissue sample. The method of the invention has hepatotropic, and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug toxicity, drug efficacy and drug metabolism. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX

SQ Sequence 176 BP; 54 A; 23 C; 23 G; 75 T; 0 U; 1 Other;

Query Match 30.7%; Score 148.4; DB 6; Length 176;
Best Local Similarity 95.6%; Pred. No. 1.6e-17;

Matches 152; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 310 TTATTTTTTAAGGAACACAAATTAAGTGTTCACCTGTGGCAAATTTGTACTTTCTCCCT 369
Db 176 TTATTTTTTAAGGAACACAAATTAAGTGTTCACCTGTGGCAAATTTGTACTTTCTCCCT 117
Qy 370 GAATTATGTTGTATCAAAGAAAAAATTTGGGAAGCATGGCAAATATCATCAAACTGA 429
Db 116 GAATTATGTTGTATCAAAGAAAAAATTTGGGAAGCATGGCAAATATCATCAAACTGA 57
Qy 430 AACTAGAATTAACTAAATTAATAAAAAAAAAAAAAA 468
Db 56 AACTAGAATTAAACANAATAATTAATAAATAAAAA 18

RESULT 5

ABL33696Xc

ID ABL33696 standard; DNA; 6668 BP.

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AC ABL33696;

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DT 26-MAR-2002 (first entry)

XX

DE Human immune system associated gene SEQ ID NO: 1669.

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KW Human; immune system disease; cytosine methylation; antiasthmatic;

KW antiarteriosclerotic; antianaemic; cytostatic; nootropic;

KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;

KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;

KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;

KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;

KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;

KW ds.

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OS Homo sapiens.

XX

PN WO200200928-A2.

XX

PD 03-JAN-2002.

XX

PF 02-JUL-2001; 2001WO-EP007537.

XX

PR 30-JUN-2000; 2000DE-01032529.

PR

01-SEP-2000; 2000DE-01043826.

XX

PA (EPIG-) EPIGENOMICS AG.

XX

PI Olek A, Piepenbrock C, Berlin K.

XX

DR WPI; 2002-130909/17.

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PT Nucleic acid comprising fragment of chemically modified gene, useful for

PT diagnosis and treatment of diseases associated with abnormal cytosine

PT methylation.

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PS Claim 1; SEQ ID NO 1669; 32pp + Sequence Listing; German.

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CC The present invention provides a number of human immune system associated

CC genes which are modified by the methylation of cytosines. The sequences

CC can be used in the diagnosis and treatment of immune system disorders,

CC including eye diseases such as retinopathy, neovascular glaucoma and

CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid

CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,

CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel

CC diseases. The present sequence is a gene of the invention

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SQ Sequence 6668 BP; 1628 A; 328 C; 1974 G; 2737 T; 0 U; 1 Other;

Query Match 15.2%; Score 73.4; DB 6; Length 6668;

Best Local Similarity 51.7%; Pred. No. 0.00041;

Matches 167; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

Qy 162 AACCTCCAGAACTGTGATCCAAATGCATATGTATCTTTGGAAGAACTCTGAAGTAAAG 221
Db 5831 AACATAATACGATAAATAAATATATATAAACACAAAAAACAACAAACAAA 5772